Percent Similarity: 38.83%   Conservative: 23
Best Local Similarity: 26.60%   Mismatches: 66
Query Match: 8.91%   Indels: 50
DB: 1   Gaps: 8

US-09-252-991A-26292 (1-245) x US-09-252-991A-5802 (1-735)

```
Qy   3 ThrSerThrCysGlyAlaIleProArgProValGlyLysTyrGlyAlaAlaGlyArgAla  22
         :::||:||:|::||| |||                             :::
Db  43 TCATCTTCCTGTCATGCCTTCGTCTTCCCCTCACGCTCTTTTACACTG-------  90

Qy  23 AspGluArgHisArgAlaAlaAspAlaSerProGlyGlyLysGlyTyrSerAlaLeuAspAspGln  42
         |||                                           |||||
Db  91 ------CGGCCAACCCAACCACCGGACCCGCGCTCCAATGCCCATCGCCACGGCGAACAG  144

Qy  43 LysAlaArgGluValMetLeuGlyLeuValAlaThrGlyGlnLeuThrAspProGluSer  62
         ||||||:||::|:::
Db 145 CCTGCCGCCCAA------------------CCGCGCACCAAGCCTGCTGAG  177

Qy  63 AlaArg--GlyLysLeuLeuGlnThrAlaLeuHisLeuPheArgSerLysGlyTyrGlu  81
         |||        ||       ||||||||||||:::
Db 178 GTTCGTCGGAGGAACTGATGGGCGGCGGCCAGCAACTGTTCCTAGACAAGGGTGTGGAC  237

Qy  82 ArgThrThrValArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePheHis 101
         ||||||:||::|:::||||
Db 238 GCCACCACCATCAGCGACGACATCGTCGCTCCCGGGGTCGCCAAGGGTACCTTCTATCAC  297

Qy 102 HisPheLysSerLysAspGluIleLeuArgSerValMetGluGlu---ThrIleLeuTyr 120
         |||:||||||||||:||:||||::||::   |::|
Db 298 TACTTCCAAGCCAAGGACGAACATCCTCTGGCCCTACGAGGCGCTTCACCAGGCTTTC  357

Qy 121 AsnThrAlaLeuMetArgAlaAlaAlaLeuAla---AspAlaGluAspLeu--------- 135
         :::        |||    |||
Db 358 CACCAGCGCCATCCGCAATGCCCGTCGAGCCTGTCCGGGAACGACCA-TCCCGCCGCGCCT  416

Qy 136 ---------ArgGluArgValLeuGlyLeu-----------IleArgCys 145
                  |||||||||||               ||||:
Db 417 GCCGGCCTGGACCGAGACGGCCCGGCGCTACCTGATGGGGCTACCGGCTGCACGAGTGT  476

Qy 146 GluLeuGln----------------------- 148
         ||||||||
Db 477 GGTCTACAGCGAGCGACCACCATCACCACCAGGCGCCAACCAGGAGCGGGACCACGGCTGCTGGA  536

Qy 149 SerIleMetGlyGlyThrGlyGlu 156
         :::||| |||||||||||
Db 537 GCAATTGGCGGAGCTACTGGAGAGA  560
```

RESULT 15
US-09-252-991A-7944
Sequence 7944, Application US/09252991A
Patent No. 6551795

Alignment Scores:
Pred. No.:   0.179   Length: 576
Score: 111.00   Matches: 42
Percent Similarity: 44.16%   Conservative: 26

Best Local Similarity: 27.27%   Mismatches: 68
Query Match: 8.87%   Indels: 18
DB: 1   Gaps: 6

US-09-252-991A-26292 (1-245) x US-09-252-991A-7944 (1-576)

```
Qy  60 ProGluSerAlaArg--------------------GlyLysLeuLeuGlnThrAlaLeuHisLeu  74
         |||||:|:                        ::|||||||:: |||
Db  38 CCGGCAGCAGGCGCCGTTCCAGCGAGTTGGGTGGGGGCGGCCATCGTTGGAGGGCGCGGTTCAGGTT  97

Qy  75 PheArgSerLysGlyTyrGluArgThrThrValArgAspLeuAlaSerAlaValGlyIle  94
         ||||::||||||:::|||
Db  98 CTGGCCAGCCAAGGCGCGCAACGTTTCACCACCGGCGTGGCCGGCGCGGGGGTG  157

Qy  95 GlnSerGlySerIlePheHisHisPheLysSerLysAspGluIleLeuArgSerValMet 114
         ||||||:||:|||||||
Db 158 AGCATCGGTTCGTCTGTACCAGTATTTCCCGAACCAAGGCGGGATCCTTCGCCGCCTGCAA  217

Qy 115 GluGluThrIleLeuTyrAsnThrAlaLeuMetArgAlaAlaAlaLeuAlaAspAla----- 132
         ::: |||::|||:||:|||  ||| |||
Db 218 AGCGACGAGTGGCGCGTGCGCCACCACGCGCTCGCTCCGGGAGATCCTCGAGGACACCGCCCGG  277

Qy 133 -------GluAspLeuArgGluValLeuGlyLeuIleLeuArg--------CysGluLeu 147
                ||| |||||| |||||||  :::|||        ||||||
Db 278 CCGCCGCTGGACGCGTTGGCCCGGGTGGTGCTCTGGCATTCGTCGCGTCGGAGTGCGAAGAG  337

Qy 148 GlnSerIleMetGlyLysGlyThrGlyGluAlaMetAlaValLeu-----ValTyrGluTrp 165
         ::|||       :|||    |||            ||||||
Db 338 GCGGCGGATACGGCGTTGGCGTCGAGCGACGCGCGGCTGTATCGGCGGACGCCGACGAGGCG  397

Qy 166 ArgSerLeuSerAlaGluGly--GlnAlaTyrIleLeuGlyLeuArgAspIleThrTyrGlu 184
         ||| ||||||||||||:: ::: |||||||||:||:::
Db 398 CGGGAGGTGAAGGCGGAGAGCGGGCGCGGGGTGTTCTCGGGGAGGCCTTGGCG  457

Qy 185 GlnMetTrpLeuAspValLeuGlyLeuAlaArgLeuAlaGly 198
         |||||||||||:
Db 458 GAGGTC--------GCCGAGGCCGAGCCGCAGCCCTGGGCCGGC  490
```

Search completed: April 29, 2003, 16:15:09
Job time : 5087 secs

RESULT 13
US-09-252-991A-5493
; Sequence 5493, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5493
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5493

Alignment Scores:
Pred. NO.:
Score: 0.206
Score: 112.00
Percent Similarity: 35.29%
Percent Identity: 21.08%
Query Match: 8.95%

Length: 693
Matches: 43
Conservative: 29
Mismatches: 92
Indels: 40

Query Match: 8.99%
DB:

US-09-252-991A-26292 (1-245) x US-09-252-991A-7804 (1-702)

Indels: 31
Gaps: 9

Qy   60 ProGluSerAlaArg----------------------GlyLysLeuLeuGlnThrAlaAlaHisLeu 74
         ||||:|| |||:|||:||:::||
Db   112 CCGGCAGCCAGCCCGTTCCACCGAGTTGGTGGCGACCATCCTCGGCGGCGGCGGCTGTTCAGGTT 171

Qy   75 PheArgSerLysGlyTyrGluArgThrThrValArgAspLeuAlaSerAlaValGlyIleGlySer 94
         |||:||:|||:||| |||||: ||| |||
Db   172 CTGGCCAGCCAGAAGGCCCGCAACGTTTCACCACCGCCGGCGTGGCCGAGGCGCCGGCGGTG 231

Qy   95 GlnSerGlySerIlePheHisHisPheLysSerLysAspGluIleLeuArgSerValMet 114
         ||||||:||| |:|||:|||::||::||| |||:
Db   232 AGCATCGGTTCGCTCGTACCAGTATTTCCCGAACAAGGCGGCGATCCTCTTCCGGCTGCAA 291

Qy   115 GluGluThrIleLeuTyrAsnThrArgAlaAlaLeuMetArgAlaAlaLeuAlaAspAla---- 132
         :|: ||| |||:|::||||| :||
Db   292 AGCGACGAGTGGGGCGGCCACCACGGCTTCGTCGGCGACCATCCTCGAGGACACCGGCCG 351

Qy   133 ------------GluAspLeuArgGluArgValLeuGlyLeuIleLeuArg---------CysGluLeu 147
               |||| |||:||||| :|: |||
Db   352 CCGCGCGCTGGACGCGGCTTGCGCCCGGCGTGGTGGCTGGCCGGCTTCGTCGGCGACTGCGAAGAG 411

Qy   148 GlnSerIleMetGlyGlyThrGlyGluAlaMetAlaValLeu----ValTyrGluTrp 165
         :|:|| :|:||| |||
Db   412 GCGCGCGGATACGGGTGGCGCTGAGCGACGCCGCGCCGACGCCGAGGCG 471

Qy   166 ArgSerLeuSerArgLeuGly---GlnAlaTyrIleLeuGlyLeuArgAspIleTyrGlu 184
         ||| ||| |:: |||||:|||: |||
Db   472 CGGGAGGTGAAGGCCGGAGGCGGCCGGTGTTCTCCGGGAGGCCTTGCCG 531

Qy   185 GlnMetTrpLeuAspValLeuGlyGluAlaArgLeuAlaGlyTyrCysGlnGlyAspPro 204
         ::|:||| |||||||||||||:|||
Db   532 GAGGTC--------GCCGAGGCCGAGGCCAGCCTGGCCGGC 564

Qy   205 PheIleLeuArgArgPheLeuThrGlyAlaLeuSerTrpThrThrThrThrPhe------ 222
                 ||:|||| |||
Db   565 --------GACTTGCTCACCACCACCCTCGCGGCGTCGGCAAGCAGTTCTCCGAA 612

Qy   223 ArgProGluGlyProMetSerLeuAspGlnLeuAlaGluGluAlaLeuAla 239
         |||:::::::|| ||| |||
Db   613 CAGCCGGCCGGAGGCGGAGGCGAGATCCAGCGGTTACGCT---GAGGCCCTGGCC 660

RESULT 14
US-09-252-991A-5802
; Sequence 5802, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5802
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5802

Alignment Scores:
Pred. NO.:
Score: 0.246
Score: 111.50

Length: 735
Matches: 50

DB:

US-09-252-991A-26292 (1-245) x US-09-252-991A-5493 (1-693)

Gaps: 5

Qy   59 AspProGluSerAlaArgGlyLysLeuLeuGlnThrAlaAlaHisLeuPheArgSerLys 78
         ||| ||| ||:||| |||
Db   73 GATTCTGAAAAAAACCCGTACGGCCCATCCTCGGCGGCGGCGGCAACGTGTTCTTGGAAAAG 132

Qy   79 GlyTyrGluArgThrThrValArgAspLeuAlaSerAlaValGlyIleGlnSerGlySer 98
         |||:||: ||| ||| |||:
Db   133 GGGGTGTCCCATACCAGCCGTGGAAACAGATCGCCAGGGCGTGACCGGTGGGCGC 192

Qy   99 IlePheHisHisPheLysSerLysAspGluIleLeuArgSerValMetGluGluThr--- 117
         :|| |||||| |:::::||
Db   193 GTCTACTCGGCCACTTCCAGAACAAGGCCCACCTGTTCAACGAGATGCTCAACCAGGTACGC 252

Qy   117 ------------------------IleLeuTyrAsnThrArgAlaAlaLeuMetArgAlaAlaLeuAlaAspAlaGluArgGlu 137
                                 ||||||:: ||| :::
Db   253 CTGCCCCGGCAGCAACTCACCCAGCGCGCCTTCGGCGTCGGATGGCAGCACCGGCTTCGCG 312

Qy   138 ArgValLeuGlyLeuIle------ArgCysGluLeuGlnSerIleMetGlyGlyThrGly 155
         |||||| ||: ||| :||
Db   313 TCGCTCTACGACCTTCGTCGGCGACTGCGAATCAGTTGCTGACGGCAGGAGAAGCCC 372

Qy   156 GluAlaMetAlaValLeuValTyrGluTrpArgSerLeuSerArgLeuGlyGlnAlaTyr 175
         ||| ::: ||| ::: |||
Db   373 CGGATCCGTGACCATCCTGATGACAACGTTGCGAATTCACCGAG--------- 414

Qy   176 IleLeuGlyLeuArgAspIleTyrGluGlnMetTrpLeuAspValLeuGlyGluAlaArg 195
         ||| ||| |||||||||||||:|||
Db   415 -------------GAACTGCGCGAGGCGCAGGAACCGCAGAACCAACGCCTTC 450

Qy   196 LeuAlaGlyTyrCysGlnGlyAspProPheIleLeuArgArgPheLeuThrGly--Ala 214
         |||:|| ||| |||
Db   451 GTGCAGATGTTCATCGGAACTCTCGAGGCCGAGCAGTTGTTC------GCCCGCGGACGAATGGCGT 504

Qy   215 LeuSerTrpThrThrThrThrPheArgProGluGlyProMetSerLeuAspGlnLeuAla 234
         ||| |||
Db   505 GTCCGGCGTGCATCCGGGCGATGACCCGAGGATGCGCCTCGCGGCGCCTTGCACGGCGTGATC 564

Qy   235 GluGluAlaLeu 238
         |||
Db   565 CTGGGCCTGTTCAACGACTGGTTGCGGCACCGCGCCGTGTTCGACCCGGATACGGACGCG 624

Db   625 GAACACCTGCTG 636

```
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9166
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9166

Alignment Scores:
Pred. No.:
Score:                    0.0709
                          113.50
Percent Similarity:       36.65%          Length:        423
Best Local Similarity:    22.36%          Matches:        36
Query Match:              9.07%           Conservative:   23
DB:                       1               Mismatches:     57
                                          Indels:         46
                                          Gaps:            3

US-09-252-991A-26292 (1-245) x US-09-252-991A-9166 (1-423)

Qy   44 AlaAlaArgGluValMetLeuGlyLeuValAlaThrGlyGlnLeuThrAspProGluSerAla   63
        ||||||||::|
Db  384 GCCCGGAGCCTTCGGCGCCCGAGATGATC-------------------------GAGGAAACC  349

Qy   64 ArgGlyLysLeuLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTyrGluArgThr      83
        ||||||                               |||
Db  348 CGCGCCAAGCTGCTGCAGACGGCCGCGCACCTGTTCCGCAAGAAGGGCTACGCGCGCACC     289

Qy   84 ThrValArgAspLeuValAlaSerAlaValGlyIleGlnSerGlySerIlePheHisHisPhe  103
        :::||                           |||          |||||||||||
Db  288 TCGATGGACGAACTGACCGCCCAGCGCCGCGCCTTCACCCCGCTGTATCACCACTTC        229

Qy  104 LysSerLysAspGluIleLeuLeuArgSerValMetGluGluThrIleLeuTyrAsnThrAla  123
        :::|||          ||:::::::           |||:::::||
Db  228 GGCGACGAAGAAAGGCCTGCCGCGCGGGGTGGTGCACGAGATCGACGAGGAGATGAGAAGATCTT 169

Qy  124 LeuMetArgAlaAlaLeuAlaAspAlaLeuGluAspLeuArgGluArgValLeuGlyLeuIle  143
        :::          |||||||
Db  168 CGCCTCGGCGCGCGCCATCCTGGCTGCCGCGCGAGGACCTC-                       133

Qy  144 ArgCysGluLeuGlnSerIleMetGlyGlyThrGlyGluAlaMetAlaValLeuValTyr     163
        |||
Db                                                                    133

Qy  164 GluTrpProArgSerLeuSerAlaGluGlyGlnAlaTyrIleLeuGluGlyLeuArgAspIleTyr 183
                     |||    :::|||||:::
Db  132 ---TCGAGCGCGGCTTCCGTGCCTACACACCGGGCCTACCTG-                      97

Qy  184 GluGlnMetTrpLeuAspValLeuGlyValAlaArgLeuAlaGlyTyrTyrCysGlnGlyAsp  203
        :::|||          |||                  |||        |||||
Db   96 ---GAAATGGCCCTCGGAAGCGGA-AATCCAGGCCATCGGTCCTGCGCGATGCCCCGGCCAT   41

Qy  204 Pro  204
        |||
Db   40 CCT   38
```

RESULT 11
US-09-252-991A-1993
; Sequence 1993, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A

```
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1993
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1993

Alignment Scores:
Pred. No.:
Score:                    0.146
                          113.50
Percent Similarity:       50.98%          Length:        654
Best Local Similarity:    34.31%          Matches:        35
Query Match:              9.07%           Conservative:   17
DB:                       1               Mismatches:     27
                                          Indels:         23
                                          Gaps:            4

US-09-252-991A-26292 (1-245) x US-09-252-991A-1993 (1-654)

Qy   66 LysLeuLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTyrGluArgThrThrVal     85
        ||||||:::||                          |||          |||||||||||
Db   64 GAGATTCTCGAATACCGCCCTCAAGCTGTTCCTCGAACACGGGGAAGACAGCCGTAACGGTC  123

Qy   86 ArgAspLeuValAlaSerAlaValGlyIleGlnSerGlySerIlePheHisHisPheLysSer  105
        :::::|||          |||          |||
Db  124 GAGATGATCGCGGAATGCCGTTCGGCGCATCGGCAAAGCCACGATCTACAAGCACTTCAAGTCC 183

Qy  106 LysAspGluIleLeuLeuArgSerValMetGluGluThrIleLeuTyrAsnThrAlaLeuMet  125
        |||          :::|||                  |||          |||
Db  184 AAGGCGGAGGAGATCTACCTCCGCCGCGTGATGCTGGAC------------TACGAGCGCGGATCTC-- 231

Qy  126 ArgAlaAlaLeuAlaAspAlaLeuGluLeu--ArgGluArgValLeuGlyLeuIleArg      144
        ||||||:::||          |||:::::
Db  232 --GCCGCGCCTGTTCCATTCCGAAGACGTTAGCCCCGACGACAAG--------------------- 270

Qy  145 CysGluLeuGlnSerIleMetGlyGlyThrGlyGluAlaMetAlaValLeuValTyrGlu     164
        |||:::::::
Db  271 --------------------GAAGCCCTGTCGCGCGGCCCCTACTTCGAG               297

Qy  165 TrpArg  166
        :::|||
Db  298 TTCCGC  303
```

RESULT 12
US-09-252-991A-7804
; Sequence 7804, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7804
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7804

```
Alignment Scores:
Pred. No.:
Score:                    0.193
                          112.50
Percent Similarity:       41.62%          Length:        702
Best Local Similarity:    26.40%          Matches:        52
                                          Conservative:   30
                                          Mismatches:     84
```

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8914
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8914

```
Alignment Scores:
Pred. No.:
Score:                     0.0953
                          115.50
Percent Similarity:        42.25%
Best Local Similarity:     25.67%
Query Match:                9.23%
DB:

Length:        618
Matches:        48
Conservative:   31
Mismatches:     67
Indels:         41
Gaps:            8
Query Match:     1
```

US-09-252-991A-26292 (1-245) x US-09-252-991A-8914 (1-618)

```
Qy   44 AlaAArgGluValMetLeuGluLeuValAlaThrGlyGlnLeuThrArgAspProGluSerAla 63
         ||||||||        |   ::||
Db   31 GCCCGCAAGCCTCGCCGCCGAGATGATC----------------------GAGGAAACC 66

Qy   64 ArgGlyLysLeuLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTyrGluArgThr 83
         ||| |||||||       |||   |||
Db   67 CGCGGCAAGCTCGATCGACGCGCCGGCCACGGCCGTTCGGCGACAACGGCTACGCCGCGGCC 126

Qy   84 ThrValArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePheHisHisPhe 103
         :||||::||       ||||| :::::::::::||||
Db  127 TCCGATGGACGAACTGACCCGCCACCGCCGCCGCCGCTCGTATCACCACTTC 186

Qy  104 LysSerLysAspGluIleLeuArgSerValMetGluGluThrIleLeuThrTyrAsnThrAla 123
         |||||||         ||||
Db  187 GGCGACAAGAAAGGCCTGCTCGCCGCGGTGGTTCCAGCAGATCGACGAGGAATGAAATCTT 246

Qy  124 LeuMetArgAlaAlaLeuAlaAspAlaGluAspLeu--------------------- 135
         :::  ||     |||||||
Db  247 CGCCTCCGGCCGCCATCCTGCTCGCCGCGGAGGACCTCTCGGAGGGGTTCCGTGCCTACAAC 306

Qy  136 ArgGluArgValLeuGlyLeuIleArgCysGluLeuGlnLeuSerIleMetGlyGlyThrGly 155
         |||
Db  307 CGGGCCTACCTGGAAATGGCCCTGGAAGCGGAAATCCAGGCAATCGTC------CTGCCC 360

Qy  156 GluAlaMetAlaValLeu------------ValTyrGluTrpArgSerLeuSer 169
         :::                             ||| ||||||
Db  361 GATGCCCCCGGCCATCCTCGGCACCGGCAGCCGACCGCTGCCTAAGC 420

Qy  170 Ala---GluGlyGlnAlaTyrIleLeuGlyLeuArgAspIleTyrGluGlnMetTrpLeu 188
         |||      |||  |||||||
Db  421 TCGATGACCGGCAA------CTGCGCCGAACTGATGGACAGC-------- 456

Qy  189 AspValLeuGluGlyLeuAlaArgLeuAlaGlyTyrTyrCysGlnGlyTyrAspProPheIleLeuArg 208
         ||| |||       ||| |||
Db  457 -------------GGGGGCGGTCCGC------ 492

Qy  209 ArgPheLeuThrGlyAlaLeu 215
         ||| ||||||||||
Db  493 TGGCTGCTCAACGGCGGCGCTG 513
```

; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10401
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10401

```
Alignment Scores:
Pred. No.:
Score:                     0.113
                          114.00
Percent Similarity:        40.57%
Best Local Similarity:     25.47%
Query Match:                9.11%
DB:

Length:        588
Matches:        54
Conservative:   32
Mismatches:     54
Indels:         72
Gaps:            9
Query Match:     1
```

US-09-252-991A-26292 (1-245) x US-09-252-991A-10401 (1-588)

```
Qy   61 GluSerAlaArgGlyLysLeuLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTyr 80
         :::               |||||||||         ||||||     |||
Db   52 CAGAAGACCCGCGCGCGGCGTATCGTCCAGGAGAGGCTGCCGGCGGCTGTTCCGCCAGGACGGCGTC 111

Qy   81 GluArgThrThrValArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePhe 100
         |||          ||||          |||:::||||
Db  112 GGCGCCACCGGCGGCTGCAACCGGCCTCGATGAAGAGGCCCTGGGCGCTGACCCATGCGGGCTTCTAC 171

Qy  101 HisHisPheLysSerLysAspGluIleLeuArgSerValMetGluGluThrIleLeuTyr 120
         |||||||||||||||     |||
Db  172 GCGCACTTCAAGTCCAAGGACGACCTGGTG------------------ 216

Qy  121 AsnThrAlaLeu----------MetArgAlaAlaLeuAlaAspAlaGluAspLeuArg 136
         ::: |||          |||||::||||     ||||
Db  217 CATGCCGCCGGCGCCAACTCGACGAAATCACCGCCCCTGGCGACGGAGGCCGGAA-------- 267

Qy  137 GluArgValLeuGlyLeuIleLeuArgCysGluLeuGlnLeuSerIleMetGlyGlyThrGlyGlu 156
         |||                                              CGA
Db  268 CGA 270

Qy  157 AlaMetAlaValLeuValTyrGluTrpArgSer--------------- 167
         :::|||:||       |||
Db  271 CCGCTGGCCGTGCTGATAGAGCAGTACCGTCTCCGCGGGATAACCCGCGGCC 330

Qy  168 -------------LeuSerAlaGluGlyGlnAlaTyrIleLeuGlyLeuArg--- 180
         |||||||         |||
Db  331 GGCTGCCGTTGCCGACCGCTGTCGCGGCGAA----CTCGGCCAGGCGCGGC 375

Qy  181 -------AspIleTyrGluGlnMetTrpLeuAspValLeuGluGlyLeuGlyAla 194
         |||         |||
Db  376 ACGGCGGAGGCCCGACCACCAGCAGCGATCGTGCCGGCCAAGCGCGTGGGCGATGATC---GAAGCG 432

Qy  195 ArgLeuAlaGlyTyrTyrCysGlnGlyTyrAsp---ProPheIleLeuArgArgPheLeuThrGly 213
         ||| |||           |||
Db  433 GCCCTGGAGGGCGGAGGACCGCAGGCCGCCGCCTGCGCCTTCGCTCGGTGTGGCGGC 492

Qy  214 AlaLeuSerTrpThrThrThrThrThrThrTrpPheArgProGluGlyProMetSerLeuAspGlnLeu 233
         ||||||                    :::
Db  493 GCGCTGCAACTGTCGGCGACGCAGC--------------GTG 516

Qy  234 AlaGluGlyLeuAlaLeuAlaLeuAlaLeuValIleLeuLysSerAspAla 245
         ::||||||||||||||:::                     ||| |||
Db  517 CAGGATGAGGCGCTGTCGCAACGACTACTCGGAAACG 552
```

PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3541
TYPE: DNA
LENGTH: 1074
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3541

Alignment Scores:

Pred. No.:		Length:	1074
Score:	0.0183	Matches:	54
	131.00	Conservative:	24
Percent Similarity:	41.94%	Mismatches:	60
Best Local Similarity:	29.03%	Indels:	48
Query Match:	10.46%	Gaps:	8
DB:	1		

US-09-252-991A-26292 (1-245) x US-09-252-991A-3541 (1-1074)

```
Qy   63  AlaAlaArgGlyLysLeuLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTyrGluArg  82
          :::|||    :||||||: |||||||  |||
Db 1011  TCCGCGACGAGCTTTCCCAGCGGCCCTGCGCGCACCTTGCGGCTACGGGCTACCACGGC  952

Qy   83  ThrThrValArgAspLeuValAlaValGlyIleGlnSerIleGlySerIlePheHisHis  102
          ||||||:|||    |:|||: :|||  |:|||   |||
Db  951  ACCACCAAGGACATGCTGTCCACCGCCTGCGGCTTGACCAAGGCCTCGTTCTACCACCAT  892

Qy  103  PheLysSerLysAspGluIleLeuArgSerValMetGluGluThr------------  117
          :|:  ||:|||:   |||   |||||   |||
Db  891  TACCCGAACAAGGAAGCCTTGCTCCGGACGACGTTCTCGAATGGACACCACCAGCGGCTCGCC  832

Qy  118  ---------IleLeuThrTyrAsnThrAlaLeu-------------------  124
                   |||  |||   :::
Db  831  GAGACGTCTTCAGCATCGCCTACGACCCCGTCGACGCGCCGAGCGGCCTGGAAAAA  772

Qy  125  ------MetArgAlaLeuAlaLeuAlaAspAlaGlyLeuAlaArgGlyValLeuGlyLeu  142
                |||        :|||   |||  :|||
Db  771  CTCGGCCCCAAGGCGCCCGGTTGTTCAGGACGACGCCATCGGCTGCTGCCTGATGGGCGTG  712

Qy  143  Ile-------------------ArgCysGluLeu---------GlnSerIleMet  151
          :|:                  |:|||         ::|
Db  711  GTCGGCGTTCGAGCGCCCACGTATGGCTCGCAGCGACGCTGAGCGCCGCAGTTCCTC  652

Qy  152  GlyGlyThrGlyLeuAlaMetAlaValAlaLeuValThrTyrGluTrpArgSerLeuSerAlaGlu  171
          ::|||  |||   |||   ||||
Db  651  GACGACTGGCGCGGCAAGCCTTCGCCCAGCTC------TACCGCCCCGCCTTCGACGAG  601

Qy  172  GlyGlyGlnAlaTyrIleLeuGlyLeuArgAspIleTyrGluGlnMetTrpLeuAspProValLeu  191
          |||||:                 |:|||    :::|||
Db  600  GCCGAGGCGCCTGGAGCGGCGGC------CGGCAACTGGTGGCTGATTTCGAA  556

Qy  192  GlyLysGluAlaArgLeuAla----------GlyTyrCysGlnGlyAspProPhe  205
          ||||||                         :|:|||
Db  555  GGCGCCCATCCTGCTGGGCGGCGAGCCGGGCCTATATCGANGGC------  505

Qy  206  IleLeuArgArgPheLeu  211
          ::|  ||||||  |||
Db  504  GTCACCCCGGCGACGGCTG  487
```

RESULT 7
US-09-252-991A-8799
Sequence 8799, Application US/0925299lA
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8799
TYPE: DNA
LENGTH: 906
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8799

Alignment Scores:

Pred. No.:		Length:	906
Score:	0.14	Matches:	54
	117.00	Conservative:	36
Percent Similarity:	38.46%	Mismatches:	82
Best Local Similarity:	23.08%	Indels:	62
Query Match:	9.35%	Gaps:	9
DB:	1		

US-09-252-991A-26292 (1-245) x US-09-252-991A-8799 (1-906)

```
Qy   18  AlaAlaLeuGlyArgAlaAlaAspGluArgHisAlaArgAlaAlaAlaAspAspProGluLysGlyTyrSer  37
          ::|||||||:|  |||   ::|
Db   20  TCGGCTGGCCGGCCGCTCCAGCGGCGGAACCGGCGACGACGGGACGAGAAGACAAATTCACATACGGCT  79

Qy   38  AlaLeu----------------------------  39
          :|||
Db   80  GCGTATGTCAAAAAATCATTGAGACATACGGCGACGTATGTCAATTATCCTGAAGCCCCTTC  139

Qy   40  --------AspAspGlnLysAlaArgGluValMetGluGluValAlaAlaThrGlyGln  56
                  ::|   |||||  :|| :::|
Db  140  GCCACCCGGAGACCTGCGATGGCCCCAAGCCTCGGCGCCGAGATGATC---  187

Qy   57  LeuThrAspProGluSerAlaArgGlyLysLeuLeuGlnThrAlaAlaHisLeuPheArg  76
                 |||||   |||   |||  |||
Db  188  ----------GAGGAAACCCGGCCGCCCAAGCTAGTGACCGGCATGGAAAGGCGTTCGCC  235

Qy   77  SerLysGlyTyrGluArgThrThrValArgAspLeuValAlaValGlyIleGlnSer  96
          :|:|||       |||    :|||  ||||
Db  236  GACAACGGCTACGCGCGGCGGCCTTCGATGGACGAAACTGACCCCGCCGGCCTCACCCGC  295

Qy   97  GlySerIlePheHisHisPheLysSerLysAspGluIleLeuArgSerValMetGluGlu  116
          ||:|||                  |||    |||
Db  296  GGCGGCCTGTATTCACCACTTCGGCGACAAGAAAGGCCTGCTCCGGACGTTGGTGCAG  355

Qy  117  ThrIleLeuThrTyrAsnThrAlaLeuMetArgAlaLeuAlaLeuAlaAspAlaGlyLeu  135
                 |||    :::|||
Db  356  ATCGACGACGAGATGAAATCTTCGCCCTCGGCGTGCCGGCGGAGGAGACCCTCTGG  415

Qy  136  ------ArgGluArgValLeuGlyLeuIleLeuArgCysGluLeuGln  148
                |||  :::|||   |||
Db  416  AGCGGCTTCGGTGCCTTACAACCGGCGCCTACCTGGAAATGGCCGGAAAATCCAG  475

Qy  149  SerIleMetGlyGlyThrGlyLeuAlaMetAlaValAlaLeu-----------Val  162
          |||                    :||||||
Db  476  CGCATCGTC----CTGCCGGATCGCCCCGGCCCATCCTCGGCAGCGACGCCGAGGCC  529

Qy  163  TyrGluTrpArgSerLeuSerAla---GluGlyGlnAlaTyrIleLeuGlyLeuArgAsp  181
          :::                     |||   ||||||
Db  530  AGCCAACTGCGCGTGCCTAAGCTCGATGACCGGGCAA------CTGCGCGGAA  574

Qy  182  IleTyrGluGlnMetTrpLeuAspProValLeuGlyLysGluAlaArgLeuAlaGlyTyrCysGln  201
          :::|||                          |||
Db  575  CTGATGGACAGC----------------GGGCCGCGTCGGC  601

Qy  202  GlyAspProPheIleLeuArgArgPheLeuThrGlyAlaLeu  215
          |||         |||   ||||||:|||
Db  602  ACGGACGCCGAGGCCCGTGGCCTGCTCAACGGCGGCGTG  643
```

RESULT 8
US-09-252-991A-8914
Sequence 8914, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

```
Pred. No.:
Score:                              0.000958         Length:                 732
Percent Similarity:                 145.00           Matches:                66
Best Local Similarity:              37.65%           Conservative:           27
Query Match:                        26.72%           Mismatches:             78
DB:                                 11.58%           Indels:                 77
                                    1                Gaps:                   11

US-09-252-991A-26292 (1-245) x US-09-252-991A-10194 (1-732)

Qy      2 ProThrSerThrCysGlyAlaIleProArgProValGlyLysTyrGlyAlaAlaGlyArg 21
            ||||||||||||:::|||
Db     10 CCGACGGCGGCTCTTGTGAGGGGCTTGCCACGC------------AGCGGGCCT 48

Qy     22 AlaAspGluArgHisArgAlaAlaAspProGluLysGlyTyrSerAlaLeuAspAsp 41
            ||||||||||                |||||::::|||
Db     49 TGC-------CGGCAC---GCTGCGTGGCGCCCGCCCCGCCATTCGAGGAGCCTCATG------ 93

Qy     42 GlnLysAlaArgGluValMetLeuGlyLeuValAlaThrArgGlyGlnLeuThrAspProGlu 61
            ::::: |||          |||||||||||
Db     94 CGCCCTACCAAAGAA------------------------------GACGGCGAA 117

Qy     62 SerAlaArgGlyLysLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTyrGlu 81
            |||||     |||||||||
Db    118 CAGACCGCGCCTCAAGATCATCGCCGGCTTCGAGCTGTTCAGGAGCAAGGGCTATTCG 177

Qy     82 ArgThrThrValArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePheHis 101
            |||||||||||                  ::: |||
Db    178 AACACACCCCTGGGCATGATCGGCCGAGGCCCGGCCGTTCACCCGTGCCGGATTCTTACTGG 237

Qy    102 HisPheLysSerLysAspGluIleLeuArgSerValMetGlyGluThr- 121
            ::::: ||          |||||||||||
Db    238 CACTTCAAGAGCAAGGACGAG------------------------------ 258

Qy    122 ThrAlaLeuMetArgAlaAlaLeuAlaAspAlaGluArgValLeuGly 141
            |||     |||||||||
Db    259 ------CTGTACGAAGCGGTGCTGGCCTACTCCCAGGAGCAGCTGATCGAA 312

Qy    142 LeuIleArgCysGluLeuGlnSerIleMetGlyGlyTyrThrGlyValAlaMetAlaValLeu 161
            |||     |||||||
Db    313 ------------CAGAGTCGCCAGTGTGGCCCGGTAGCCCGGCCTCGCCGTGGAGACACTTC 360

Qy    162 ValTyrGluTrpArgSerLeuSerAlaGluGlyGlnAlaThrTyrIleLeuGlyLeuArgAsp 181
            |||                                         |||
Db    361 GTCGGCGGAATCGTTTCGCCTCGCTGCTGGACCAGCGCCTGGGTTATCG-GCCAGTCCTTCGAGAT 419

Qy    182 IleTyrGluGlnMetTrpLeuAsp 189
            ||||||
Db    420 CCTGCTGACAA------------------------------GACCGACTCACCGCGCCAGATGGCGGAGCCACCCTGAAACG 470

Qy    190 ------------------------------ValLeuGlyValAlaArgLeuAlaGlyTyr 199
                                              |||||::: |||
Db    471 CGAAGGCAAGCTCACCCGTGCCATGGTGCACTTGCTGGAGAGCTGAT------------------------------ 518

Qy    200 CysGlnGlyAspProPheIleLeuArgArgPheLeuThrGlyAlaLeuSerTrpThrThr 219
            |||                  |||||||
Db    519 TGCCAAGGC------------------------------GCACGCGGATGAAGGATCGGCGCGATCACTGGCCTTGCT 566

Qy    220 ThrTrpPheArgProGluGly 226
            ||| |||||:::|||
Db    567 GCTCTATTCGAGGCCTGATGGG 587
```

```
Alignment Scores:
Pred. No.:
Score:                              0.008            Length:                 651
Percent Similarity:                 131.00           Matches:                54
Best Local Similarity:              41.94%           Conservative:           24
Query Match:                        29.03%           Mismatches:             60
DB:                                 10.46%           Indels:                 48
                                    1                Gaps:                   8

US-09-252-991A-26292 (1-245) x US-09-252-991A-3553 (1-651)

Qy     63 AlaArgGlyLysLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTyrGluArg 82
            :::|||          |||||
Db    109 TCCCGGCGACGAGCGTTCTCCAGGGCGCCGGCCACCTTCCGTGCGCTACGGCTATTCGGGC 168

Qy     83 ThrThrValArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePheHisHis 102
            |||||||||                  ::: ||||||
Db    169 ACCACCATGGACAATGCTCGTCCAGGCCCCGGCCGTTGACCAAGGCCTCGTTCTACCACCAT 228

Qy    103 PheLysSerLysAspGluIleLeuArgSerValMetGlyGluThr- 117
            ::::::|||||        |||::::|||
Db    229 TACCCGAACAAGAAGAGCCTTGCTCCGGACGTTCTCGAATGAACCACCAGCGGCGCTCGCC 288

Qy    118 ------------------------------IleLeuTyrAsnThrAlaLeu 124
                                              |||
Db    289 GAGACGCTCTTCAGCATCGCCTACGACCCCGCTGCTGACGCCCCGGCGACCGGCTGGAAAA 348

Qy    125 ------MetArgAlaAlaLeuAlaAspAlaGluArgValLeuGlyLeu 142
                                  ::::|||||
Db    349 CTCGGCCCGCAAGGCCGCCCCGGTGTTGCTCCAGGACGAACAGCATCGGCGTCGCCGTG 408

Qy    143 IleArgCysGluLeu------GlnSerIleMet 151
            ||| |||::: ||
Db    409 GTCGGCGGTTCGAGCCCAGCTATGGTCTCGAGCGAAGGGCGCGGAGCTTTCTC 468

Qy    152 GlyGlyTyrThrGlyValAlaMetAlaValLeuValTyrGluTrpArgSerLeuSerAlaGlu 171
            |||||        :::|||
Db    469 GACGACTGGGCGCGAAGCCTTCGGCCCAGCTC--------------------TACCGCCCGGCCTTCGACGAG 519

Qy    172 GlyGlnAlaThrTyrIleLeuGlyLeuArgAspIleTyrGluGlnMetTrpLeuAspValLeu 191
            |||||:::|||                  |||:::
Db    520 GCGCAGGCGGCCTGGAGCGGCGGGC------------CGGCAACTGGGTGGCCTGAATTTCGAA 564

Qy    192 GlyGluAlaArgLeuAla------------------------------GlyTyrCysGlnGlyAspProPhe 205
            |||||                             |||||
Db    565 GCGGCCATCCTCCTTCGGCGCGCCATCTATGGCGAGCCGGGCTATATCGATGGC--------- 615

Qy    206 IleLeuArgArgPheLeu 211
            ||| |||
Db    616 GTCACCCGGCGAGCGGCTG 633
```

Db 181 GAAAGCCCCGGCAAGCTGCTGCAGACACCGCCGCCGCCCACCTGTTCCGCAGCAAAGCTAC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   81 GluArgThrThrValArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePhe 100

Db 241 GAACCCACACGGTCGCGACAGACCTGCTGCCGCAGCAGGCGTGGGCATCCAGTCAGCANTTC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 101 HisHisPheLysSerLysAspGluIleLeuLeuSerValMetGluGluThrIleLeuTyr 120

Db 301 CATCACTTCAAGAGCAAGGATGAGATCCTCCTGTCGGTGATGGAAGAGACCATCCTCTAC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 AsnThrAlaLeuMetArgAlaAlaLeuAlaAspAlaGluLeuArgGluArgValLeu 140

Db 361 AACACCGCCCTGATGCGCGCGCCCTGGCCGACGCCGAGCTGCGCGAACGCGGGTGCTG 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 141 GlyLeuIleArgCysGluLeuGlnSerIleLeuMetGlyGlyThrGlyGluAlaMetAlaVal 160

Db 421 GGACTGATCCGCTGCGAGCTGCAAATCGATCATGGCGGTACCGGCGAGGCGATGGCGGTG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 161 LeuValTyrGluTrpArgSerLeuSerAlaGluLeuGlnAlaThrTyrIleLeuGlyLeuArg 180

Db 481 CTGGTCTACGAGTGGCGCAGCCTCTCGGCCGAGCTCCAGGCGACCTACATCCTCGGCCTGCGC 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 181 AspIleTyrGluGluLeuLeuArgPheLeuThrGlyAlaLeuSerTrpThrThrThr 200

Db 541 GACATCTACGAGGAGCTGCTGCGCTTCCTGACCGGTGCGCTGTCCTGGACCACCACC 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 201 GlnGlyAspProPheIleLeuArgArgArgLeuThrArgGlyLeuArgLeuAlaGlyTyrCys 220

Db 601 CAGGGCGACCCGTTCATCCTGCGGCGGCGCCTTCCTCACCCGCGGCCTGCGGCTGGCCGGCTACTGC 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 221 TrpPheArgProGluGlyProMetSerLeuAspGlnLeuAlaLeuGluAlaLeuAla 240

Db 661 TGGTTCCGTCCGGAAGGACCCATGAGCTCTCGATCAGCTCGCCCTGGGCGTG 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 241 ValIleLysAspAla 245

Db 721 GTGATCAAAGGACGCC 735

RESULT 2
US-09-252-991A-9640
; Sequence 9640, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9640
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9640

Alignment Scores:
Pred. No.:
Score: 1.02e-11
Score: 250.00   Length: 402
Percent Similarity: 100.00%   Matches: 47
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 19.978%   Mismatches: 0
DB: Indels: 0
                                          Gaps: 0

US-09-252-991A-26292 (1-245) x US-09-252-991A-9640 (1-402)
Qy   1 MetProThrSerThrCysGlyAlaIleProArgProValGlyLysTyrGlyAlaAlaGly 20

Db 261 ATGCCGACAAGCACTTCGCGGGGCGGCCAATCCCGAGCCGGTCGGCGGGAAATACGGACGGGCCGGG 320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   21 ArgGlaAspGluArgHisArgAlaAlaLeuAspAlaAspProGluLysGlyLysTyrSerAlaLeuAsp 40

Db 321 CCGCGGATGAGCGGCACCAGACGCCGCCCGACGATCCGGAAAAAGGGGTACTCAGCGTTGGAC 380
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   41 AspGlnLysAlaArgGluVal 47

Db 381 GATCAGAAAGCCCCGGAAGTG 401

RESULT 3
US-09-252-991A-9616/c
; Sequence 9616, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9616
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9616

Alignment Scores:
Pred. No.:
Score: 4.22e-08
Score: 216.00   Length: 2064
Percent Similarity: 100.00%   Matches: 40
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 17.25%   Mismatches: 0
DB: Indels: 0
                                          Gaps: 0

US-09-252-991A-26292 (1-245) x US-09-252-991A-9616 (1-2064)
Qy   1 MetProThrSerThrCysGlyAlaIleProArgProValGlyLysTyrGlyAlaAlaGly 20

Db 122 ATGCCGACAAGCACTTCGCGGGGCGGCCAATCCCGAGCCGGTCGGCGGGAAATACGGACGGGCCGGG 63
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   21 ArgAlaAspGluArgHisArgAlaAlaAspAspProProGluLysGlyLysTyrSerAlaLeuAsp 40

Db   62 CCGCGGCGGATGAGCGGCACCAGACGATCCGGAAAAAGGGGTACTCACCGTTGGAC 3

RESULT 4
US-09-252-991A-10194
; Sequence 10194, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10194
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10194

Alignment Scores:

OM protein - nucleic search, using frame_plus_p2n model

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GenCore version 5.1.4_p5_4578

Run on: April 29, 2003, 14:50:22 ; Search time 5082 Seconds
                       1.617 Million cell updates/sec

Title: US-09-252-991A-26292
Perfect score: 1252
Sequence: 1 MPTSTCGAIPRPVGKYGAAG...........GPMSLDQLAEEALALVIKDA 245

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop   6.0 , Fgapext 7.0
                Delop   6.0 , Delext   7.0

Searched: 16571 seqs, 16774251 residues

Total number of hits satisfying chosen parameters: 33142

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL-frame+_p2n.model -DEV-soft -Q-allen991.pep -DB-6551795.seq -SUFFIX-pto
-OUT-align.26292 -MINMATCH-0.1 -LOOPCL-0 -LOOPEX0-0 -UNITS-bits -START-1
-END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45 -MODE-LOCAL -OUTFMT-pto
-THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto
-NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000 -NCPU-6 -NO_XLPXY
-NEG_SCORES-0 -LONGLOG -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

Database :   6551795.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES:

Result No.	Score:	% Query Match	Length DB ID	Description
1	1252	100.0	738 US-09-252-991A-9721	Sequence 9721, Ap
2	250	20.0	402 US-09-252-991A-9640	Sequence 9640, Ap
3	216	17.3	2064 US-09-252-991A-9616	Sequence 9616, Ap
4	145	11.6	732 US-09-252-991A-7804	Sequence 7804, Ap
5	131	10.5	651 US-09-252-991A-10194	Sequence 10194, A
6	131	10.5	1074 US-09-252-991A-3553	Sequence 3553, Ap
7	117	9.3	906 US-09-252-991A-3541	Sequence 3541, Ap
8	117	9.3	618 US-09-252-991A-8799	Sequence 8799, Ap
9	115.5	9.2	618 US-09-252-991A-8914	Sequence 8914, Ap
10	114	9.1	588 US-09-252-991A-10401	Sequence 10401, A
11	113.5	9.1	423 US-09-252-991A-9166	Sequence 9166, Ap
12	113.5	9.1	654 US-09-252-991A-1993	Sequence 1993, Ap
13	112.5	9.0	702 US-09-252-991A-7804	Sequence 7804, Ap
14	112	8.9	693 US-09-252-991A-5493	Sequence 5493, Ap
15	111.5	8.9	735 US-09-252-991A-5802	Sequence 5802, Ap
16	111	8.9	576 US-09-252-991A-7944	Sequence 7944, Ap
17	111	8.9	642 US-09-252-991A-11468	Sequence 11468, A
18	111	8.9	747 US-09-252-991A-11489	Sequence 11489, A
c 19	111	8.9	2430 US-09-252-991A-16171	Sequence 16171, A
c 20	110.5	8.8	615 US-09-252-991A-13547	Sequence 13547, A
c 21	110.5	8.8	924 US-09-252-991A-13900	Sequence 13900, A
c 22	109.5	8.7	618 US-09-252-991A-8221	Sequence 8221, Ap
22	109	8.7	654 US-09-252-991A-8152	Sequence 8152, Ap
23	106.5	8.5	1515 US-09-252-991A-2038	Sequence 2038, Ap
24	106	8.5	852 US-09-252-991A-16108	Sequence 16108, A
25	105.5	8.4	579 US-09-252-991A-3573	Sequence 3573, Ap
26	103	8.2	558 US-09-252-991A-3119	Sequence 3119, Ap
27	103	8.2	654 US-09-252-991A-13115	Sequence 13115, A
28	103	8.2	708 US-09-252-991A-16416	Sequence 16416, A
29	102.5	8.2	606 US-09-252-991A-14319	Sequence 14319, A
c 30	102.5	8.2	687 US-09-252-991A-14385	Sequence 14385, A
31	102.5	8.2	1584 US-09-252-991A-5646	Sequence 5646, Ap
32	100.5	8.0	813 US-09-252-991A-3162	Sequence 3162, Ap
33	97	7.7	1311 US-09-252-991A-8437	Sequence 8437, Ap
34	96	7.7	717 US-09-252-991A-8505	Sequence 8505, Ap
c 35	95.5	7.6	1533 US-09-252-991A-16493	Sequence 16493, A
c 36	95.5	7.6	1380 US-09-252-991A-11242	Sequence 11242, A
37	94	7.5	1632 US-09-252-991A-11015	Sequence 11015, A
c 38	93.5	7.5	939 US-09-252-991A-4182	Sequence 4182, Ap
c 39	93.5	7.5	477 US-09-252-991A-7606	Sequence 7606, Ap
c 40	93.5	7.5	615 US-09-252-991A-4366	Sequence 4366, Ap
c 41	93.5	7.5	696 US-09-252-991A-4282	Sequence 4282, Ap
c 42	93.5	7.5	702 US-09-252-991A-5549	Sequence 5549, Ap
43	93.5	7.5	1203 US-09-252-991A-15742	Sequence 15742, A
44	93	7.4	834 US-09-252-991A-1968	Sequence 1968, Ap
45	93	7.4	858 US-09-252-991A-2132	Sequence 2132, Ap

ALIGNMENTS

RESULT 1
US-09-252-991A-9721
; Sequence 9721, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMON/
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9721
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9721

Alignment Scores:
Pred. No.:   2.87e-83
Score: 1252.00   Length: 738
Percent Similarity: 100.00%   Matches: 245
Percent Identity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 1   Indels: 0
DB: Gaps: 0

US-09-252-991A-26292 (1-245) x US-09-252-991A-9721 (1-738)

Qy   1 MetProThrSerThrCysGlyAlaIleProArgProValGlyLysTyrGlyAlaAlaGly 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGCCGACAAGCACTTGCGGCGCCATCCCAAGGCCGGTCGGCAAATACGGAGCCGCCGGG 60

Qy   21 ArgAlaAspGluArgHisArgAlaAlaAspAspProGluLysGlyTyrSerAlaLeuAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CGCGCGGATGAGCCGCCACCGAGCCCCCGACGATCCGGAAAAGGGGTACTCGGCGTTGGAC 120

Qy   41 AspGlnLysAlaAlaArgGluValMetLeuGluLeuValAlaThrGlyGlnLeuThrAspPro 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GATCAGAAAGCCCCGGAAGTGATGCTGGAACTGGTGGCTACCGGACAGCTCACCGATCCG 180

Qy   61 GluSerAlaAArgGlyLysLeuLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTyr 80

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 30, 2003, 06:59:07 ; Search time 0.001 Seconds
                                          (without alignments)
                                          147.980 Million cell updates/sec

Title: US-09-252-991A-26292
Perfect score: 1252
Sequence: 1 MPPSTCGAIPRPVGKYGAAG..........GPMSLDQLAEEALVIKDA 245

Scoring table:
               BLOSUM62
               Xgapop 10.0 , Xgapext 0.5
               Ygapop 10.0 , Ygapext 0.5
               Fgapop 6.0 , Fgapext 7.0
               Delop   6.0 , Delext   7.0

Searched: 1 seqs, 302 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=soft -Q=allen991.pep -DB=us-09-966-608-1
-SUFFIX=pto -OUT=align_26292_1 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPXY
-NEG_SCORES=0 -LONGLOC -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   us-09-966-608-1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

                                  %
Result   Query
No.   Score Match Length DB ID   Description
----- ----- ----- ------ -- -------------- -----------
  1   429   34.3   302   1   us-09-966-608-1

ALIGNMENTS

RESULT 1
us-09-966-608-1

Alignment Scores:
Pred. No.:   0
Score: 429.00
Percent Similarity: 94.00%
Best Local Similarity: 84.00%
Query Match: 34.27%

                    Length: 302
                    Matches: 84
                    Conservative: 10
                    Mismatches: 6
                    Indels: 0
                    Gaps: 0

Qy 107 AspGluIleLeuArgSerValMetGluGluThrIleLeuTyrAsnThrAlaLeuMetArg 126
        |||||||||||||||||||||||||||||||||| |||||||| ::|||||||||
Db   62 GATGAGATATTGCGTCGCGTGATGGAGGAGAAACCATCACAACACCGGATGATGCGC 121

Qy 127 AlaAlaLeuAlaAspAlaGluAspProLeuArgGluArgValLeuGlyLeuIleArgCysGlu 146
        ||:::|||||||| ::|||||||||||||||||||||||||||||||||||||||||
Db 122 GCTTCACTGGAGGAGGGCGGACAGCGACGGGTGCCGCGAACGCCGTGCTGGCGCGTGATATCCGGTCCGGAG 181

Qy 147 LeuGlnSerIleMetGlyGlyThrGlyGluAlaMetAlaValLeuLeuValTyrGluTrpArg 166
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 182 TTGCAGTCGATCATGGGCGGCGCAGTGGCCATGGCCGTGCTGCTGGTGTACGAATGGCGC 241

Qy 167 SerLeuSerAlaGlyGluGlyGlnAlaTyrIleLeuGlyLeuArgAspIleTyrGluGlnMet 186
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Db 242 TCGCTGTCGGCCGGCGAAGGCCAGGCGCACGTGCTCGGCCTCCGGGACGTGTATGAGCAGATC 301

Search completed: April 30, 2003, 06:59:07
Job time : 0.001 secs

US-09-252-991A-26292 (1-245) x us-09-966-608-1 (1-302)

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Db   2 GATCTGGCCAGCGCCGTGGGCATCCAGTCCGGCAGCATCTTTCATCACTTCAAGAGCAAG 61